

# SEQUENCE LISTING

<110> Bayer Aktiengesellschaft

<120> Ligand binding domains of Ultraspiracle (USP) proteins

<130> Le A 34 772

<140>

<141>

<150> DE 100 36 461.6

<151> 2000-07-25

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 262

<212> PRT

<213> Heliothis virescens

<400> 1

Val	Gln	Glu	Leu	Ser	Ile	Glu	Arg	Leu	Leu	Glu	Met	Glu	Ser	Leu	Val
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Ala	Asp	Pro	Ser	Glu	Glu	Phe	Gln	Phe	Leu	Arg	Val	Gly	Pro	Asp	Ser
			20					25						30	

Asn	Val	Pro	Pro	Lys	Phe	Arg	Ala	Pro	Val	Ser	Ser	Leu	Cys	Gln	Ile
			35				40					45			

Gly	Asn	Lys	Gln	Ile	Ala	Ala	Leu	Val	Val	Trp	Ala	Arg	Asp	Ile	Pro
	50					55				60					

His	Phe	Ser	Gln	Leu	Glu	Met	Glu	Asp	Gln	Ile	Leu	Leu	Ile	Lys	Gly
65						70				75				80	

Ser	Trp	Asn	Glu	Leu	Leu	Leu	Phe	Ala	Ile	Ala	Trp	Arg	Ser	Met	Glu
				85					90					95	

Phe	Leu	Thr	Glu	Glu	Arg	Asp	Gly	Val	Asp	Gly	Thr	Gly	Asn	Arg	Thr
			100					105						110	

Thr	Ser	Pro	Pro	Gln	Leu	Met	Cys	Leu	Met	Pro	Gly	Met	Thr	Leu	His
			115					120				125			

09909556-072001

Arg Asn Ser Ala Leu Gln Ala Gly Val Gly Gln Ile Phe Asp Arg Val  
130 135 140

Leu Ser Glu Leu Ser Leu Lys Met Arg Thr Leu Arg Val Asp Gln Ala  
145 150 155 160

Glu Tyr Val Ala Leu Lys Ala Ile Ile Leu Leu Asn Pro Asp Val Lys  
165 170 175

Gly Leu Lys Asn Arg Gln Glu Val Glu Val Leu Arg Glu Lys Met Phe  
180 185 190

Leu Cys Leu Asp Glu Tyr Cys Arg Arg Ser Arg Ser Ser Glu Glu Gly  
195 200 205

Arg Phe Ala Ala Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Ser  
210 215 220

Leu Lys Ser Phe Glu His Leu Phe Phe Phe His Leu Val Ala Asp Thr  
225 230 235 240

Ser Ile Ala Gly Tyr Ile Arg Asp Ala Leu Arg Asn His Ala Pro Pro  
245 250 255

Ile Asp Thr Asn Met Met  
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<210> 2

<211> 466

<212> PRT

<213> *Heliothis virescens*

<400> 2

Met Ser Val Ala Lys Lys Asp Lys Pro Thr Met Ser Val Thr Ala Leu  
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Ile Asn Trp Ala Arg Pro Leu Pro Pro Gly Gln Gln Gln Gln Pro Met  
20 25 30

Thr Pro Thr Ser Pro Gly Asn Met Leu Gln Pro Met Ala Thr Pro Ser  
35 40 45

Asn Leu Pro Thr Val Asp Cys Ser Leu Asp Ile Gln Trp Leu Asn Leu  
50 55 60

Glu Gly Gly Phe Met Ser Pro Met Ser Pro Pro Glu Met Lys Pro Asp

65

70

75

80

Thr Ala Met Leu Asp Gly Leu Arg Asp Asp Ser Thr Pro Pro Pro Ala  
85 90 95

Phe Lys Asn Tyr Pro Pro Asn His Pro Leu Ser Gly Ser Lys His Leu  
100 105 110

Cys Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr Gly Val Tyr  
115 120 125

Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp  
130 135 140

Leu Thr Tyr Ala Cys Arg Glu Glu Arg Asn Cys Ile Ile Asp Lys Arg  
145 150 155 160

Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Ala Cys  
165 170 175

Gly Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Ala Ala Arg  
180 185 190

Gly Thr Glu Asp Ala His Pro Ser Ser Ser Val Gln Val Gln Glu Leu  
195 200 205

Ser Ile Glu Arg Leu Leu Glu Met Glu Ser Leu Val Ala Asp Pro Ser  
210 215 220

Glu Glu Phe Gln Phe Leu Arg Val Gly Pro Asp Ser Asn Val Pro Pro  
225 230 235 240

Lys Phe Arg Ala Pro Val Ser Ser Leu Cys Gln Ile Gly Asn Lys Gln  
245 250 255

Ile Ala Ala Leu Val Val Trp Ala Arg Asp Ile Pro His Phe Ser Gln  
260 265 270

Leu Glu Met Glu Asp Gln Ile Leu Leu Ile Lys Gly Ser Trp Asn Glu  
275 280 285

Leu Leu Leu Phe Ala Ile Ala Trp Arg Ser Met Glu Phe Leu Thr Glu  
290 295 300

Glu Arg Asp Gly Val Asp Gly Thr Gly Asn Arg Thr Thr Ser Pro Pro  
305 310 315 320

Gln Leu Met Cys Leu Met Pro Gly Met Thr Leu His Arg Asn Ser Ala

335

Met Met  
465

4